Using Molecular Dynamics to Model the Stacking Behaviour of Perylene Bisimide Derivatives in Aromatic Solvent

M. Hollfelder, S. Gekle

published in

NIC Symposium 2016
K. Binder, M. Müller, M. Kremer, A. Schnurpfeil (Editors)

Forschungszentrum Jülich GmbH,
John von Neumann Institute for Computing (NIC),
Schriften des Forschungszentrums Jülich, NIC Series, Vol. 48,
ISBN 978-3-95806-109-5, pp. 105.
http://hdl.handle.net/2128/9842

Using Molecular Dynamics to Model the Stacking Behaviour of Perylene Bisimide Derivatives in Aromatic Solvent

Manuel Hollfelder and Stephan Gekle

Biofluid Simulation and Modeling, University of Bayreuth, 95444 Bayreuth, Germany
E-mail: stephan.gekle@uni-bayreuth.de

Using the power of present-day supercomputers makes it possible to solve Newton's equations of motion numerically, even for large systems. Molecular Dynamics provides a powerful simulation method to get insight in the behaviour of molecules under many conditions when considering atoms as charged solid spheres and hiding the quantum mechanics in effective potentials. We use this method to characterise the physical properties of different systems, e.g. polymers, water, organic and inorganic molecules.
As an example of our work, we present a model of the π-π stacking dynamics of a perylene bisimide molecule when solvated in aromatic solvents. Our calculations show that the transition from the open (unstacked) to the stacked configuration is hindered by a small free energy barrier of approx. $1\,\mathrm{k_B T}$ in the aromatic solvent toluene. The origin of this barrier is traced back to π-π interactions between perylene and the aromatic solvent which are very similar in nature to those between two PBI monomers. The stacking process proceeds in three phases via two well-defined transition states: (i) in the first phase, the two PBI molecules share part of their respective solvation shells forming the first transition state. Further approach needs to squeeze out the shared solvent layer thus creating the energy barrier. (ii) After removal of the separating solvent the two PBIs form a second transition state with one monomer located at a random position in the other's solvation shell. (iii) Finally, the two PBIs slide on top of each other into their final stacked position.

1 Introduction

Newton's equations of motion cannot be solved analytically for large systems. The term large system is, however, misleading since every system above two particles must be considered of this type. Therefore, modelling atoms as solid and charged spheres in the framework of Molecular Dynamics leads only to new results if one takes the possibility of numerical calculations into account. Nowadays supercomputers allow us to solve the equations of Molecular Dynamics simulations for truly large systems, e.g. number of atoms above $20\,000$, within finite time.

Using the computation time granted by the John von Neumann Institute for Computing (NIC) and provided on the supercomputer JUROPA at Jülich Supercomputing Centre (JSC) we model different molecules, e.g. polymers, organic and inorganic molecules, water, and derive models of interaction or calculate physical properties of these molecules. This article gives a brief summary of our work and presents as an example results obtained from numerical calculations of an organic dimer consisting of two covalently linked perylene bisimide molecules (PBM) using highly parallelised supercomputers[1].

Sec. 2 summarises the motivation of our investigations. After introducing briefly the methods in Sec. 3, we use Sec. 4.1 to characterise the structure of the solvation shell around a single PBM when solvated in toluene as a typical aromatic solvent. In Sec. 4.2 we then

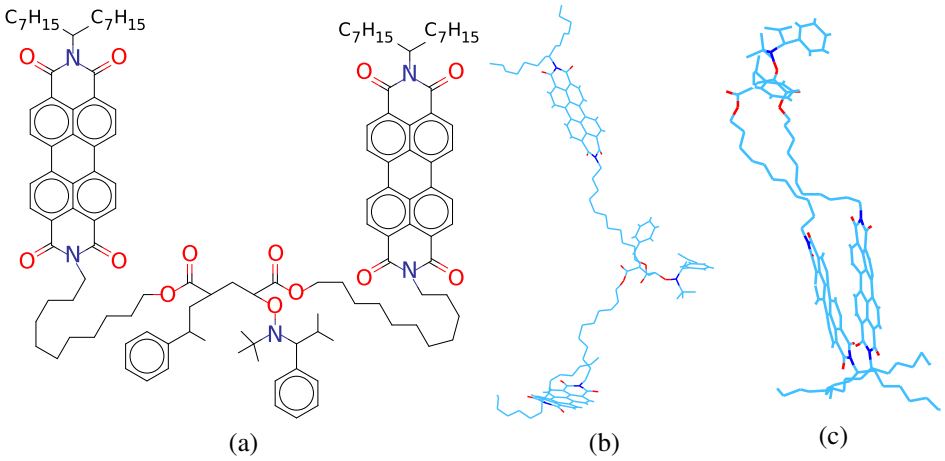


Figure 1. (a) Chemical structure of the investigated perylene bisimide dimer molecule. (b) Snapshot of an unstacked (OPEN) state and (c) snapshot of a stacked (STACK) configuration. The solvent toluene is omitted for clarity.

present the free energy profiles for the dimer solvated in toluene which governs the stacking transition. In Sec. 4.3 we describe the full stacking pathway which proceeds from the open to the stacked configuration via two well-defined transition states.

2 Motivation

Molecules based on derivatives of perylene are a widely used material for many different purposes: they have useful optical properties because their emission colour can be adjusted over a wide range of the visible spectrum, they are used as highly sensitive sensors and show n-type conduction making them suitable for organic transistors and optoelectronic devices in general. Furthermore, molecules based on perylene derivatives are considered a promising candidate for building highly efficient organic solar cells.

Given these numerous applications, perylene derivatives have been intensively investigated both experimentally and computationally in the recent past. One of their salient characteristics is a tendency to form large tower-like aggregates (stacks) of molecules as has been demonstrated by experiments and *ab initio* molecular dynamics simulations. This stacking behaviour can be traced back to the interactions of the π-orbitals and has great influence on the properties of the materials as it dramatically changes, e.g., the efficiency of energy and charge transfer processes. The static structure of these stacks has been well characterised: in the stacked state the perylenes remain mostly planar with the distance between the two planes being around $0.35\,\mathrm{nm}$; the perylene axes are tilted by approx. $45°$ with respect to each other and the free energy gained from stacking is of the order of $15\,\mathrm{kJ/mol}$ depending on the exact chemical structure of the perylene derivative as determined by linear free energy relationships in conjunction with UV/Vis spectroscopy[2].

A systematic investigation of the dynamic transition pathway from the open (unstacked) to the stacked state, however, has not been conducted so far. Here, we have

investigated the transition dynamics considering a perylene bisimide dimer solvated in toluene by Molecular Dynamics (MD) simulations. The investigated structure consists of two perylene bisimide monomers (PBM) and is shown in Fig. 1 (a). Both monomers are connected by an alkane chain containing furthermore oxygen, nitrogen and two aromatic rings. On the other side of the PBM two C_7H_{15} chains are present. We consider the solvent toluene representing a prototypical aromatic solvent. The toluene-solvated system has recently been investigated by fluorescence spectroscopy[3,4]. The unstacked (OPEN) and stacked (STACK) configurations are well reproduced by our MD simulations as shown in Fig. 1 (b) and (c). We find the distance of the planes defined by the (almost perfectly) planar PBMs to be $0.36\,\mathrm{nm}$ which is in good agreement with values obtained from experiments and earlier MD simulations[5].

3 Simulation Methods

Classical Molecular Dynamics simulations were run with Gromacs and the Gromos 53a6 force field was used. This means that the parameters of the bonds, harmonic spring constants, Lennard-Jones parameters etc. follow a parameter set of typical bonding values and interactions which is itself consistent. Building new molecules reduces to combining the correct parameters for the bonds between the atoms and assigning charges to the atoms. These force field topologies were automatically calculated for the perylene derivatives using *Automated Force Field Topology Builder (ATB) and Repository*. The force field file for the solvent toluene was calculated using PRODRG. United-atom force field topologies were used for the simulations which means that hydrogen atoms and carbon atoms, e.g. for alkane chains, are combined to super-atoms to reduce the necessary computation time. The visual analysis of the molecular structure files and trajectories was carried out using VMD.

For the simulations the dimer was solvated in a rectangular box with 1000 toluene molecules. After energy minimisation and NVT equilibration, the final runs were simulated as NPT ensembles at $300\,\mathrm{K}$ and $1\,\mathrm{bar}$. In order to investigate the general behaviour and stacking of the dimer, simulations were started with different starting configurations of the atoms' positions and velocities. Every simulation was stopped as soon as stacking occurred.

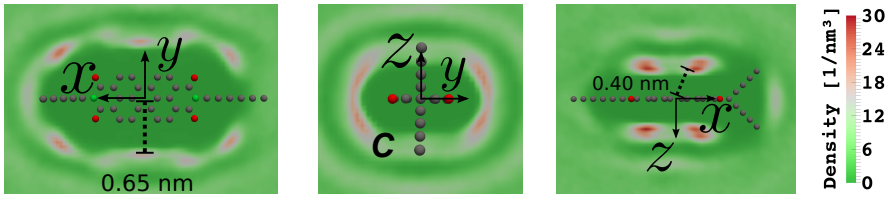
For the free energy calculations in Sec. 4.2 we use umbrella sampling where the distance between the centres of mass of the PBMs was chosen as a reaction coordinate and different states along that coordinate were created using the Gromacs pull code. After equilibration the simulations were simulated as NPT ensembles for each window at $300\,\mathrm{K}$ and $1\,\mathrm{bar}$. For the bias potential the *umbrella potential* implemented in the Gromacs package was used and simulations with different spring constants were started. The free energy profile was calculated using the *Weighted Histogram Analysis Method* implemented in Gromacs as *g_wham*.

4 Results and Discussion

4.1 Static Solvation Shell for Toluene

We first analyse the static structure of the toluene solvation shell around a single PBM of the dimer in the OPEN state. We find a clear first solvation shell whose time averaged

density is, however, rather inhomogeneous as shown in Fig. 2 from different perspectives. Since the monomers are fairly stiff they remain almost perfectly planar during the entire simulation time.



(a) (b) (c) (d)

Figure 2. Average density of the solvent toluene around one PBM of the dimer during the OPEN state. The density is illustrated as coloured plots over planar cuts through the PBM centre of mass along the xy (a), yz (b), and xz (c) plane with the legend of the plots in (d). The PBM's carbon, oxygen, and nitrogen atoms are depicted in grey, red, and green, respectively. In (b) *C* marks a special point which is referred to during the stacking mechanism in Sec. 4.3.

In Fig. 2 (a), which corresponds to a view from the top, alternating regions of high and low densities can be distinguished. The distance from the monomer's centre of mass (COM) to the high density spots on the y-axis is approximately $0.65\,\mathrm{nm}$. Near the partially charged oxygen atoms we observe regions of fairly low solvent density. In Fig. 2 (b), which represents a head-on view, one can see two rather homogeneous ellipsoidal rings formed around the monomer by the solvent. The side view, Fig. 2 (c), illustrates four clear spots of high solvent density right above and below the PBM. The distance between the spots right above and below the PBM and the PBM itself is in z-direction $0.40\,\mathrm{nm}$ corresponding to the well-known stacking distance between perylene molecules. This confirms the existence of a π-π-interaction between the perylene and the aromatic solvent very similar in nature to the π-π interaction in perylene stacks. This interaction strongly influences the stacking dynamics as we will show further below.

4.2 Free Energy of Stacking

As a first step towards understanding the stacking pathway of the dimer in aromatic solvent, we present in Fig. 3 the free energy profile as a function of the distance between the COMs of the two monomers for toluene. The profiles are calculated using umbrella sampling as described in the methods section. Any stacking pathway needs to proceed from the plateau region at the right of Fig. 3 corresponding to the OPEN state towards the minimum located at $0.38\,\mathrm{nm}$ corresponding to the STACK state at the very left. Note that the distance between the COM considered here is slightly larger than the plane-plane distance of $0.36\,\mathrm{nm}$ in the STACK state due to the tilting of the monomers with respect to each other.

There is a clear energy barrier with a height of approx. $1\,\mathrm{k_B T}$ separating the STACK and OPEN states from each other in the solvent toluene. The barrier is rather broad, starting at $1.40\,\mathrm{nm}$ and extending down to $0.8\,\mathrm{nm}$. From the top of the barrier the free energy drops sharply towards its minimum. Around $0.50\,\mathrm{nm}$ we observe a turning point marking

a change in the curvature of the free energy curve. Finally, for distances smaller than $0.38\,\mathrm{nm}$ the free energy rises steeply which is caused by unfavourable squeezing of the PBMs during the stacked state.

The free energy difference between the minimum identified with the STACK state and the OPEN state with constant free energy for distances beyond $1.40\,\mathrm{nm}$ is approximately $5.2\,\mathrm{k_B T}$ corresponding to $13\,\mathrm{kJ/mol}$. This is in good agreement with values obtained from UV/Vis experiments for the aggregation of perylene bisimide: for a slightly different structure of the PBMs (two additional benzene molecules and no connecting carbon chain) the free energy change was obtained as $15.8\,\mathrm{kJ/mol}$ for the solvent toluene[2].

The density profiles of the toluene solvation shells around the monomers (Fig. 2) allow a physical interpretation of the distinct features observed in the free energy profile in the transition region between $1.4\,\mathrm{nm}$ and $0.8\,\mathrm{nm}$. Noting from Fig. 2 (b) and (c) that the solvation shells are located at distances between $0.40\,\mathrm{nm}$ in z-direction and $0.65\,\mathrm{nm}$ in y-direction, the first contact of the solvation shells is expected to occur for distances between $0.8\,\mathrm{nm}$ and $1.3\,\mathrm{nm}$ (depending on the relative orientation of the PBMs during approach) which corresponds closely to the width and position of the energy barrier for toluene. After contact, further approach of the PBMs is only possible if (at least) one of the PBMs loses part of its solvation shell and the two PBMs further on "share" solvent molecules. Scraping off the solvation shell clearly requires energy in the case of the solvent toluene thus explaining the observed energy barrier. For distances smaller than about $0.7\,\mathrm{nm}$ the PBMs start interacting directly leading to a rapid drop towards the STACK state which represents the absolute minimum of the free energy.

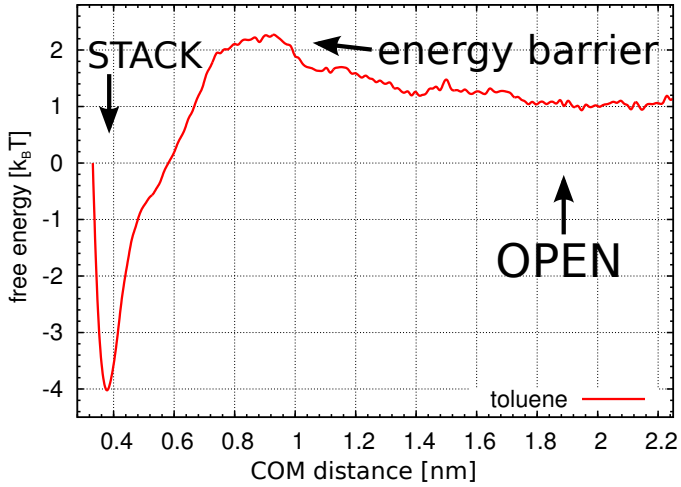
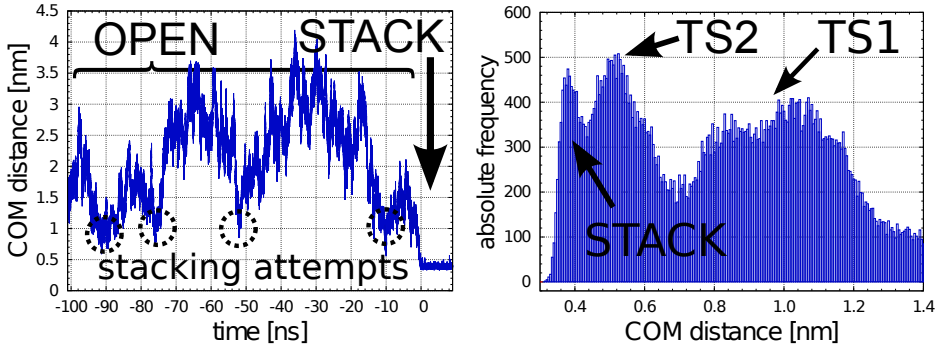


Figure 3. Free energy change as a function of the centre of mass (COM) distance between both PBMs of the dimer for the solvent toluene (red). The states STACK/OPEN and the energy barrier for toluene are marked and the energy profiles are shifted against each other for clarity.



(a) (b)

Figure 4. (a) The COM distance between both PBMs with stacking at $t = 0\,\mathrm{ns}$. The distance decreases several times to values between $0.80\,\mathrm{nm}$ and $1.00\,\mathrm{nm}$ (marked spots) without causing a change to the stacked state STACK which is characterised by an average COM distance of about $0.38\,\mathrm{nm}$. (b) Histogram over COM distances for the transition from OPEN to STACK in the solvent toluene. Only frames $< 2000\,\mathrm{ps}$ before stacking are taken into account. The peak around $1.00\,\mathrm{nm}$ corresponds to the transition state TS1, the second one around $0.50\,\mathrm{nm}$ to TS2 and the third one around $0.38\,\mathrm{nm}$ to the state STACK.

4.3 Dynamic Stacking Pathway of Perylene Bisimide in Toluene

We now turn to the actual stacking pathway for toluene as an example of an aromatic solvent. Fig. 4 (a) shows the COM distance of the two monomers as a function of time for a typical trajectory before and during the stacking process. The origin of time at $t = 0\,\mathrm{ns}$ has been located at the stacking transition which clearly separates the STACK from the OPEN configurations. Before the actual transition, however, the distance decreases several times to values between $0.80\,\mathrm{nm}$ and $1.00\,\mathrm{nm}$ but without continuing to the final stacked state. These "failed attempts" are a consequence of the energy barrier seen in Fig. 3 which can be overcome by thermal fluctuations only in a small number of cases.

We now focus more closely on the actual stacking process. The most notable feature are two regions of fairly constant COM distance during the stacking of the monomers during the simulations. These regions correspond to two well-defined transition states which we shall denominate in the following as TS1 and TS2, respectively. These transition states can be found with variable time duration in all our simulations during the stacking process. To give a full picture, we present in Fig. 4 (b) a histogram taken over all simulations during the last $2000\,\mathrm{ps}$ before stacking. The value of $2000\,\mathrm{ps}$ was estimated from the average time the stacking process lasts during the different simulations. Beside the expected peak corresponding to the STACK state at $0.38\,\mathrm{nm}$, the histogram clearly shows two further peaks: a broad first peak centred around $1.0\,\mathrm{nm}$ and a second sharper one at about $0.50\,\mathrm{nm}$. The COM distances where these peaks occur correspond to the transition states TS1 and TS2 and are evidence of the general nature of the transition states.

The picture that thus emerges is a stacking pathway consisting of three consecutive phases. In the first phase both PBMs approach each other closely until the respective solvation shells first come into contact and subsequently merge to form the first transition state TS1. In this state, which is illustrated in Fig. 5 (a), the two monomers share part of their respective solvation shell (green solvent molecules). Further approach would require the

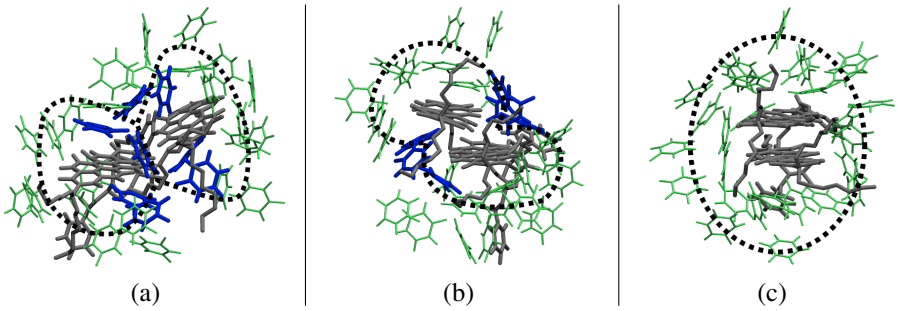


Figure 5. The different states during the stacking process illustrated with the solvation shell (dashed lines) around the PBMs. (a) View of the first transition state TS1 in which the PBMs share part of their solvation shells (shared solvent has blue colour). (b) Second transition state TS2 where the PBMs replace the solvent by themselves and only some solvent remains next to them (blue molecules) which stabilises this state. (c) Final stacked state.

complete removal of the shared solvent molecules which is connected to the energy barrier as observed in Fig. 3. In most cases, the dynamics continues without transcending the barrier and the PBMs separate again (corresponding to the "failed attempts" in Fig. 4). In some cases, however, the energy barrier can be overcome by adequate thermal fluctuations and the dynamics continues to the second phase.

In the second phase, the solvent between the PBMs is expelled, the PBMs approach more closely, and the first monomer becomes part of the second monomer's solvation shell (and *vice versa*). In TS2 there are still some solvent molecules present as shown in Fig. 5 (b) by the green solvent molecules. These stabilise TS2 by their π-π interactions with the perylene. The existence of TS2 furthermore reflects itself in the slightly flatter part of the free energy profile around $0.50\,\mathrm{nm}$ in Fig. 3. Both monomers arrange themselves such that the normal vectors to the PBM planes are parallel. For the position of the two PBMs relative to each other we find the most probable angles around $47°$ of the connecting COM and the normal vector showing that the monomers approach each other via a well-defined "channel" through the point marked *A* in Fig. 2 (b). The time span during which TS2 exists strongly varies with the second monomer's exact location and the stabilising solvent molecules. Once TS2 has been reached, however, the system is already situated on the steep downward slope of the free energy which makes final stacking inevitable.

In the third and final phase, the second monomer revolves around the first one in order to find its final stacked position with the two PBM planes lying right on top of each other, possessing the well-known COM distance of $0.38\,\mathrm{nm}$ and a joint solvation shell as shown in Fig. 5 (c).

5 Conclusion

In conclusion, we have elucidated the dynamic stacking pathway of perylene bisimide dimers solvated in toluene using Molecular Dynamics simulations in combination with free energy calculations. In toluene, the stacked and unstacked states are well separated by a free energy barrier of approx. $1\,\mathrm{k_B T}$ which is due to the fairly rigid solvation shells that the aromatic solvent forms around each perylene bisimide monomer. During the stacking

transition this barrier is overcome in three phases: (i) after the initial approach and the first contact of the solvation shells, the two monomers form a metastable first transition state (TS1) in which they share part of their respective solvation shells. Further approach requires the removal of the shared region of the solvation shell thus explaining the observed energy barrier. (ii) If thermal fluctuations allow the system to overcome this energy barrier, the system forms a second transition state (TS2) in which the interjacent solvent of the shared solvation shell is expelled and substituted by one of the perylene monomers themselves which, loosely speaking, "solvate themselves" in this state. (iii) In the last step the monomers revolve around each other until the two planes lie on top of each other which represents the final stacked configuration.

A central result of our investigations is that the stacking pathway is mainly determined by the ability of the aromatic solvent to form π-π-interactions with the solute very similar to those formed between the perylenes themselves. This leads to an energy barrier which must be overcome before the system can form the familiar stacks.

Acknowledgements

The authors gratefully acknowledge the computing time granted by the John von Neumann Institute for Computing (NIC) and provided on the supercomputer JUROPA at Jülich Supercomputing Centre (JSC).

Financial support comes from the Volkswagen Foundation in the framework of the Lichtenberg program and from the Graduiertenkolleg 1640. Further thanks are owed to Florian Spreitler, Jürgen Köhler and Mukundan Thelakkat for helpful discussions.

References

1. M. Hollfelder and S. Gekle, *Dynamic Stacking Pathway of Perylene Dimers in Aromatic and Nonaromatic Solvents*, The Journal of Physical Chemistry B, **119**, no. 32, 10216–10223, 2015, PMID: 26186499.
2. Z. Chen, B. Fimmel, and F. Würthner, *Solvent and Substituent Effects on Aggregation Constants of Perylene Bisimide π-Stacks - a Linear Free Energy Relationship Analysis*, Org. Biomol. Chem., **10**, 5845–5855, 2012.
3. F. Spreitler, M. Sommer, M. Thelakkat, and J. Köhler, *Conformational Dynamics of Di-(Perylene Bisimide Acrylate) and Its Footprints in Steady-State, Time-Resolved, and Fluorescence-Correlation Spectroscopy*, Phys. Chem. Chem. Phys., **14**, 7971–7980, 2012.
4. F. Spreitler, M. Sommer, M. Hollfelder, M. Thelakkat, S. Gekle, and J. Köhler, *Unravelling the Conformations of Di-(Perylene Bisimide Acrylate) by Combining Time-Resolved Fluorescence-Anisotropy Experiments and Molecular Modelling*, Phys. Chem. Chem. Phys., **16**, 25959–25968, Nov. 2014.
5. V. Marcon, J. Kirkpatrick, W. Pisula, and D. Andrienko, *Supramolecular Structure of Perylene Tetracarboxdiimides*, phys. stat. sol. (b), **245**, no. 5, 820–824, May 2008.